

GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: April 28, 2003, 13:48:10 ; Search time 44 seconds  
(without alignments)  
2795.235 Million cell updates/sec

Title: US-09-497-822c-19

Perfect score: 4912

Sequence: 1 MEVQLGLGRVRRPSKTYR.....SVQPKILSGKVKPIYFHTQ 923

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

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23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4880	99.3	919	18	AAW14783
2	4880	99.3	919	21	AAW78914
3	4880	99.3	919	23	AAE19061
4	4872	99.2	919	10	AAFP93109
5	4838.5	98.5	918	20	AAV33491
6	4827.5	98.3	918	12	AAV33491
7	4814	98.0	919	10	AAFP90996
8	4201.5	85.5	902	10	AAFP91006
9	4200.5	85.5	902	10	AAFP91110
10	4187.5	85.3	902	12	AAV12224

11	2429	49.5	452	20	AAV21627	Ligand binding dom
12	2401	48.9	839	23	AAG68238	Fused androgen rec
13	2029.5	41.3	388	23	ABB83821	Human androgen rec
14	1493.5	30.4	294	23	ABB83822	Human androgen rec
15	1459	29.7	630	12	AAV12230	trpe/androgen rece
16	1349.5	27.5	260	22	AAV97073	rat androgen rece
17	1337.5	27.2	576	12	AAV12229	trpe/androgen rece
18	1261	25.7	933	20	AAV21621	Ligand binding dom
19	1256	25.6	933	21	AAV97237	Human progesterone
20	1243	25.3	246	23	AAU75930	Androgen receptor
21	1212.5	24.7	250	22	AAV65959	Human androgen rec
22	1071.5	21.8	984	20	AAV21622	Ligand binding dom
23	1069.5	21.8	984	9	AAV80922	Sequence of the hu
24	1066	21.7	1070	18	AAW17789	Green fluorescent
25	1042	21.2	777	9	AAV80919	Ligand binding dom
26	1042	21.2	777	20	AAV21623	Ligand nuclear glu
27	1039	21.2	777	18	AAW44700	Androgen independe
28	838	17.1	158	21	AAV78913	Human unliganded a
29	795	16.2	154	20	AAV33504	Human progesterone
30	765	15.6	251	21	AAV36786	Rat progesterone r
31	765	15.6	255	22	AAV97074	Truncated GAL4 DBD
32	735	15.0	630	23	ABB80766	Geneswitch regulat
33	734	14.9	630	23	ABB80765	Chain A of structu
34	728	14.8	240	23	AAE17863	Geneswitch regulat
35	719	14.6	654	23	ABB80764	Chimeric Cre-LDB-G
36	675.5	13.8	667	18	AAW44701	lCre-FRT-GAP*. Sy
37	671.5	13.7	613	22	AAE47153	Chain A of structu
38	666	13.6	215	23	AAE17861	Glucocorticoid rec
39	657.5	13.4	251	21	AAV36787	Glucocorticoid rec
40	644.5	13.1	534	17	AAW03197	A rat glucocortico
41	644	13.1	284	21	AAV19249	Glucocorticoid rec
42	636	12.9	284	19	AAW45514	Glucocorticoid rec
43	636	12.9	284	19	AAV39140	Rat glucocorticoid
44	636	12.9	284	21	AAV67559	Rat glucocorticoid
45	636	12.9	284	21	AAV78898	Glucocorticoid rec

#### ALIGNMENTS

RESULT 1

AAW14783  
ID AAW14783 standard; Protein; 919 AA.

AC AAW14783;

DT 22-JUN-1997 (first entry)

XX Androgen receptor.

XX Androgen receptor; acidic fibroblast growth factor; arGF;

XX Antisense; benign prostatic hyperplasia; prostate cancer; therapy.

XX Homo sapiens.

XX WO9711170-A1.

XX 27-MAR-1997.

XX 20-SEP-1996; 96WO-US15081.

XX 20-SEP-1995; 95US-0004018.

XX (WOMC-) WORCESTER FOUND BIOMEDICAL RES.

XX Zamechnik PA;

XX WPI; 1997-202879/18.

XX N-PSDB; AAT63407.

XX Oligonucleotide(s) antisense to human androgen receptor and acidic

XX FGF genes - used to inhibit gene expression, for the treatment of

XX benign prostatic hyperplasia

XX Disclosure; Page 22-28; 51pp; English.

XX Human androgen receptor (AA14783) binds testosterone and, acting at the transcriptional level, regulates the growth of normal prostatic cells. Antisense oligonucleotides (see also AAT63200, AAT63404-05) based on an androgen receptor cDNA clone (see also AAT63407) can be used to prevent androgen receptor gene expression, thereby inhibiting the growth or survival of prostatic cells for the treatment of benign prostatic hyperplasia and prostate cancer.

XX Sequence 919 AA;

Query Match 99.3%; Score 4880; DB 18; Length 919;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 919; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

Qy 1 MEVOLGLGRVYPRPSKTYRGAFQNLFSQREVIONFPGPRHPEAASAPPGASLLLOQO 60  
Db 1 MEVOLGLGRVYPRPSKTYRGAFQNLFSQREVIONFPGPRHPEAASAPPGASLLLL-- 57

Qy 61 QO 120  
Db 58 -QO 116

Qy 121 POSALECHPERGCVPEPNAAGKLPQOLPAPDEDDSAAPSTLSLGLPTFPGLSGCS 180  
Db 117 POSALECHPERGCVPEPNAAGKLPQOLPAPDEDDSAAPSTLSLGLPTFPGLSGCS 176

Qy 181 ADKDLSEASTMQLLOQO 240  
Db 177 ADKDLSEASTMQLLOQO 236

Qy 241 LCAVSVSMGLGVEALEHLSPEQLRGDCMYAPLLGVPVAVRTPCAPLAECKSILLDS 300  
Db 237 LCAVSVSMGLGVEALEHLSPEQLRGDCMYAPLLGVPVAVRTPCAPLAECKSILLDS 296

Qy 301 AGKSTEDTARYSPFGGTYKLEGEISGCSAAGSSGTLELPSTLSLYKSGALDEAAA 360  
Db 297 AGKSTEDTARYSPFGGTYKLEGEISGCSAAGSSGTLELPSTLSLYKSGALDEAAA 356

Qy 361 YQSRDYNEFLAAGPPPPPPHPPHARIKLENPLDYGSAAAAAQAQRYGDLASLHGAG 420  
Db 357 YQSRDYNEFLAAGPPPPPPHPPHARIKLENPLDYGSAAAAAQAQRYGDLASLHGAG 416

Qy 421 AAGPGSGSPSAASSWHTLFTABEGQLYPCGGGGGGGGGGGGGGGGGGGGGGGGEAGA 480  
Db 417 AAGPGSGSPSAASSWHTLFTABEGQLYPCGGGGGGGGGGGGGGGGGGGGGGGGEAGA 476

Qy 481 VAPGYTRPPQLAGESDFTAPDWWYPGMVSRVPPSPCTCVKSEMGPMWDSYSGPYGD 540  
Db 477 VAPGYTRPPQLAGESDFTAPDWWYPGMVSRVPPSPCTCVKSEMGPMWDSYSGPYGD 536

Qy 541 MRLETARDHVLPIIDYFPQKTLICGDEASGCHYGALTGCGSKVFFKRAAEKQKYLCA 600  
Db 537 MRLETARDHVLPIIDYFPQKTLICGDEASGCHYGALTGCGSKVFFKRAAEKQKYLCA 596

Qy 601 SRNDCTIDFRKNCPSRLKRCYAGMTLGARKLKLGNLKLQFCEASSTSTSTETTT 660  
Db 597 SRNDCTIDFRKNCPSRLKRCYAGMTLGARKLKLGNLKLQFCEASSTSTSTETTT 656

Qy 661 QKTVSHIEGECQPIFLNVLIEAIPGVYACAGHNNOPDSFAALLSSLNELGERQLVHV 720  
Db 657 QKTVSHIEGECQPIFLNVLIEAIPGVYACAGHNNOPDSFAALLSSLNELGERQLVHV 716

Qy 721 KWAKALPGFNLHVDQMAVIOYSWNGLMVFAMGWSFTNVNSRMILYFAPDLVFNERYMH 780  
Db 717 KWAKALPGFNLHVDQMAVIOYSWNGLMVFAMGWSFTNVNSRMILYFAPDLVFNERYMH 776

Qy 781 KSRMYSCQVRMHLQOECGWLQITPOEFLCNKALLIESIIPVDGLKQKFFDELPMYIK 840  
Db 777 KSRMYSCQVRMHLQOECGWLQITPOEFLCNKALLIESIIPVDGLKQKFFDELPMYIK 836

Qy 841 ELDRILIAKKNPTSCSRREYQLTLLKLDVSQPIARELHQFTFDLLIKSHMVSVDPEMMA 900  
Db 837 ELDRILIAKKNPTSCSRREYQLTLLKLDVSQPIARELHQFTFDLLIKSHMVSVDPEMMA 896

Qy 901 EIISVQVPEKILSGKVKPIYPHTQ 923  
Db 897 EIISVQVPEKILSGKVKPIYPHTQ 919

RESULT 2  
AAV78914  
ID AAV78914 standard; protein; 919 AA.  
XX AC AAV78914;  
XX DT 23-MAY-2000 (first entry)  
XX DE Human androgen receptor (AR) amino acid sequence.  
XX KW Androgen receptor; AR; androgen-independent activation; inhibitor;  
KW cancer; benign prostatic hyperplasia; hirsutism; androgenic alopecia;  
KW acne; breast cancer; Kennedy disease; prostate cancer.  
XX OS Homo sapiens.  
XX PN WO200001813-A2.  
XX PD 13-JAN-2000.  
XX PF 30-JUN-1999; 99WO-CA00604.  
XX PR 30-JUN-1998; 98US-0091871.  
XX PA (UYBR-) UNIV BRITISH COLUMBIA.  
XX PI Sadar MD, Bruchovsky N, Gout PW, Snoek R, Mawji NR;  
XX WPI; 2000-182113/16.  
XX PT Novel non-androgen ligand binding peptides for inhibiting  
PT androgen-independent activation of androgen receptor, used for  
PT screening compounds and for treatment of androgen-mediated diseases.  
PT such as prostate cancer  
XX PS Disclosure; Page 7; 32pp; English.  
XX CC This sequence represents the human androgen receptor (AR) amino acid  
CC sequence. The invention relates to a fragment of the AR corresponding to  
CC amino acids 234-391 (see AAV78913). The fragment mediates  
CC androgen-independent activation of the AR. The androgen receptor acts as  
CC a transcription factor, regulating the expression of certain  
CC androgen-responsive genes. Interaction of the AR with the protein kinase  
CC A signal transduction pathway involves interaction with the androgen  
CC independent region. The AR fragment and peptides derived from it can be  
CC used as agents for inhibiting androgen independent activation of the  
CC androgen receptor, as activation domains, and as a tool for screening  
CC for compounds which affect androgen-independent activation of the AR.  
CC The peptides, when used in combination with androgen deprivation,  
CC effectively limit androgen mediated disease progression. These diseases  
CC include cancer, benign prostatic hyperplasia, hirsutism, androgenic  
CC alopecia, acne, breast cancer, Kennedy disease, and especially prostate  
CC cancer. The peptides and nucleic acids encoding them, are especially used  
CC for the treatment of androgen-mediated diseases, especially prostate  
CC tumours in patients deprived of androgen.  
XX SQ Sequence 919 AA;

Query Match 99.3%; Score 4880; DB 21; Length 919;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 919; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

Qy 1 MEVOLGLGRVYPRPSKTYRGAFQNLFSQREVIONFPGPRHPEAASAPPGASLLLOQO 60  
Db 1 MEVOLGLGRVYPRPSKTYRGAFQNLFSQREVIONFPGPRHPEAASAPPGASLLLOQO 60

```
Db 1 MEVQLGLGRVYPRPPSKTYRGAFQNLFGSVREVIONPGRHPEAASAPPGASLILL--- 57
QY 61 QQQQQQQQQQQQQQQQQQQQQQQQQQQQQETSPROQQQQQGGEDGSPQARRGPTGYLVLDDEEQPSQ 120
Db 58 -QQQQQQQQQQQQQQQQQQQQQQQQQQQQETSPROQQQQQGGEDGSPQARRGPTGYLVLDDEEQPSQ 116
QY 121 QSALECHPERGCVPEPGAAVAASKGLPQPLPAPDEDDSAAPSTLSLLGPTFFGLSSCS 180
Db 117 QSALECHPERGCVPEPGAAVAASKGLPQPLPAPDEDDSAAPSTLSLLGPTFFGLSSCS 176
QY 181 ADLKDILSEASTMOLLOQQQOEAVSESSSGRAREASGAPTSSKDNLYGTTISDNAME 240
Db 177 ADLKDILSEASTMOLLOQQQOEAVSESSSGRAREASGAPTSSKDNLYGTTISDNAME 236
QY 241 LKAVSVSMGLGVEALEHLSPEQOLRGDCMYAPLLGVPPAVRTPCAPLAECGSLDDDS 300
Db 237 LKAVSVSMGLGVEALEHLSPEQOLRGDCMYAPLLGVPPAVRTPCAPLAECGSLDDDS 296
QY 301 AGKSTEDTAESYSPFKGGYTKLGESLGCSSAAAGSGTLELPSTLSLYKSGALDEAAA 360
Db 297 AGKSTEDTAESYSPFKGGYTKLGESLGCSSAAAGSGTLELPSTLSLYKSGALDEAAA 356
QY 361 YQSRDYNNFPLALAGPPPPPPHARIKLENPLDYGSAAAAAOCRYGDLASLHGAG 420
Db 357 YQSRDYNNFPLALAGPPPPPPHARIKLENPLDYGSAAAAAOCRYGDLASLHGAG 416
QY 421 AAGPGSGSPSAAASSSWHTLFTAEQOLYGPCGGGGGGGGGGGGGGGGGGGGEAGA 480
Db 417 AAGPGSGSPSAAASSSWHTLFTAEQOLYGPCGGGGGGGGGGGGGGGGGGGGEAGA 476
QY 481 VAPGYTRPQGLAGQESDTPDVMYPCGMVSRVYPTCYKSEMGPMDSYSGPYGD 540
Db 477 VAPGYTRPQGLAGQESDTPDVMYPCGMVSRVYPTCYKSEMGPMDSYSGPYGD 536
QY 541 MRLETARDHVLPIDYPPQKTLICGDEASGCHYGALTCGCKVFFKRAAEKQKYLCA 600
Db 537 MRLETARDHVLPIDYPPQKTLICGDEASGCHYGALTCGCKVFFKRAAEKQKYLCA 596
QY 601 SRNDCTIDKFRKNCPSCLRKCYEAGMTLGARKLKLKLOEAGEASSTTSPTTEET 660
Db 597 SRNDCTIDKFRKNCPSCLRKCYEAGMTLGARKLKLKLOEAGEASSTTSPTTEET 656
QY 661 QKLTVSHIEGYEQPIFLNVLEAIEPGVVCAGHDNNQPSFAALLSSNELGERQLVHVY 720
Db 657 QKLTVSHIEGYEQPIFLNVLEAIEPGVVCAGHDNNQPSFAALLSSNELGERQLVHVY 716
QY 721 KWAKALPGFRNLHVDDQMAVIOYSWMLVYFAMGWRSTNVNSRMLYFAPDLVFNRYMH 780
Db 717 KWAKALPGFRNLHVDDQMAVIOYSWMLVYFAMGWRSTNVNSRMLYFAPDLVFNRYMH 776
QY 781 KSRMYSQVYMRHLSDQFGLWLTPOEFLCMKALLLSIIPVDGLKNOKFFDELRMNYIK 840
Db 777 KSRMYSQVYMRHLSDQFGLWLTPOEFLCMKALLLSIIPVDGLKNOKFFDELRMNYIK 836
QY 841 ELDRITACKRNKPTSCSRFYOLTLLDSVQPIARELHQFTDILLIKSHWVSDFPEMMA 900
Db 837 ELDRITACKRNKPTSCSRFYOLTLLDSVQPIARELHQFTDILLIKSHWVSDFPEMMA 896
QY 901 EILSVQPKILSGKVKPIYFHTQ 923
Db 897 EILSVQPKILSGKVKPIYFHTQ 919

RESULT 3
ID AAE19061
XX AAE19061 standard; Protein; 919 AA.
AC AAE19061;
XX
XX
DT 21-MAY-2002 (first entry)
XX
DE Human androgen receptor (AR).
XX
```

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KW Human; AIB1; amplified in breast cancer 1; androgen receptor; AR;
KW prostate cancer; chromosome X.
XX
OS Homo sapiens.
XX
PN WO200210452-A2.
XX
PD 07-FEB-2002.
XX
PF 27-JUL-2001; 2001WO-US23834.
XX
PR 27-JUL-2000; 2000US-221074P.
XX
PA (UYRP ) UNIV ROCHESTER.
XX
PI Chang C;
XX
DR WPI; 2002-206195/26.
XX
DR N-PSDB; AND30440.
XX
PT Assessing the risk of acquiring or developing prostate cancer in a
PT human subject, comprises determining the length of the contiguous CAG,
PT CAA and/or GGN repeats in the AIB1 gene and/or androgen receptor gene
PT of the subject.
XX
PS Disclosure; Page 62-63; 86pp; English.
XX
CC The invention relates to a method for assessing the risk of prostate
CC cancer in a human subject. The method involves determining the length
CC of the contiguous CAG or CAA repeats in both AIB1 (Amplified In Breast
CC cancer 1) gene alleles or contiguous CAG, CAA or GGN repeats in the
CC androgen receptor gene of the subject. The method is useful for
CC assessing a subject's risk for acquiring or developing prostate cancer.
CC The present sequence is human androgen receptor (AR) protein. Human
CC AR gene is located on X chromosome.
XX
SQ Sequence 919 AA;
XX
Query Match 99.3%; Score 4880; DB 23; Length 919;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 919; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
QY 1 MEVQLGLGRVYPRPPSKTYRGAFQNLFGSVREVIONPGRHPEAASAPPGASLILLQQQ 60
Db 1 MEVQLGLGRVYPRPPSKTYRGAFQNLFGSVREVIONPGRHPEAASAPPGASLILL--- 57
QY 61 QQQQQQQQQQQQQQQQQQQQQQQQQQQQQETSPROQQQQQGGEDGSPQARRGPTGYLVLDDEEQPSQ 120
Db 58 -QQQQQQQQQQQQQQQQQQQQQQQQQQQQETSPROQQQQQGGEDGSPQARRGPTGYLVLDDEEQPSQ 116
QY 121 QSALECHPERGCVPEPGAAVAASKGLPQPLPAPDEDDSAAPSTLSLLGPTFFGLSSCS 180
Db 117 QSALECHPERGCVPEPGAAVAASKGLPQPLPAPDEDDSAAPSTLSLLGPTFFGLSSCS 176
QY 181 ADLKDILSEASTMOLLOQQQOEAVSESSSGRAREASGAPTSSKDNLYGTTISDNAME 240
Db 177 ADLKDILSEASTMOLLOQQQOEAVSESSSGRAREASGAPTSSKDNLYGTTISDNAME 236
QY 241 LKAVSVSMGLGVEALEHLSPEQOLRGDCMYAPLLGVPPAVRTPCAPLAECGSLDDDS 300
Db 237 LKAVSVSMGLGVEALEHLSPEQOLRGDCMYAPLLGVPPAVRTPCAPLAECGSLDDDS 296
QY 301 AGKSTEDTAESYSPFKGGYTKLGESLGCSSAAAGSGTLELPSTLSLYKSGALDEAAA 360
Db 297 AGKSTEDTAESYSPFKGGYTKLGESLGCSSAAAGSGTLELPSTLSLYKSGALDEAAA 356
QY 361 YQSRDYNNFPLALAGPPPPPPHARIKLENPLDYGSAAAAAOCRYGDLASLHGAG 420
Db 357 YQSRDYNNFPLALAGPPPPPPHARIKLENPLDYGSAAAAAOCRYGDLASLHGAG 416
QY 421 AAGPGSGSPSAAASSSWHTLFTAEQOLYGPCGGGGGGGGGGGGGGGGGGGGEAGA 480
Db 417 AAGPGSGSPSAAASSSWHTLFTAEQOLYGPCGGGGGGGGGGGGGGGGGGGGEAGA 476
```



## RESULT 5

AAV33491  
 ID AAV33491 standard; Protein; 918 AA.  
 XX  
 AC AAV33491;  
 XX  
 DT 19-JAN-2000 (first entry)  
 XX  
 DE Human androgen receptor protein.  
 XX  
 KW Proapoptotic; dependence domain; p75NTR; androgen receptor; DCC;  
 KW huntingtin polypeptide; Machado-Joseph disease; SCAL; SCA2; SCA6;  
 KW atrophin-1; cell death; apoptosis; Huntington's disease; head trauma;  
 KW Alzheimer's disease; Kennedy's disease; spinocerebellar ataxia; stroke;  
 KW dentatorubropallidolysian atrophy; cell proliferation; cell survival;  
 KW neoplastic; malignant; autoimmune; fibrotic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9945944-A1.  
 XX  
 PD 16-SEP-1999.  
 XX  
 PF 11-MAR-1999; 99WO-US05250.  
 XX  
 PR 12-MAR-1998; 98US-0041886.  
 XX  
 PA (BURN-) BURNHAM INST.  
 XX  
 PI Bredesen DE, Rabizadeh S;  
 XX  
 DR WPI; 1999-561617/47.  
 DR N-PSDB; AA233424.  
 XX  
 PT New proapoptotic dependence peptides, used to develop products for  
 PT treating, e.g. Alzheimer's disease -  
 XX  
 PS Disclosure; Page 90-93; 199pp; English.  
 XX  
 CC This invention describes novel pure proapoptotic dependence peptides  
 CC which comprise a sequence of an active dependence domain selected from  
 CC dependence polypeptides consisting of p75NTR, androgen receptor, DCC,  
 CC huntingtin polypeptide, Machado-Joseph disease gene product, SCAL, SCA2,  
 CC SCA6 and atrophin-1 polypeptide. The proapoptotic peptides are capable  
 CC of inducing cell death and can be used to develop products to the severity of  
 CC inhibit apoptosis. The methods can be used for reducing the severity of  
 CC a proapoptotic dependence domain mediated pathological conditions e.g.  
 CC Huntington's disease, Alzheimer's disease, Kennedy's disease,  
 CC Spinocerebellar ataxia, dentatorubropallidolysian atrophy,  
 CC Machado-Joseph disease, stroke or head trauma. They can also be used for  
 CC reducing the severity of a pathological condition mediated by upregulated  
 CC cell proliferation or cell survival e.g. neoplastic, malignant,  
 CC autoimmune or fibrotic conditions. This sequence represents a human  
 CC androgen receptor described in the method of the invention.  
 XX

SQ Sequence 918 AA;

## Query Match

Best Local Similarity 98.5%; Score 4838.5; DB 20; Length 918;  
 Matches 914; Conservative 0; Mismatches 1; Indels 11; Gaps 2;

Qy 1 MEVQLGLGRVYPPSTKYTGAFQNLFSQSVREVIONGPRHPEAASAPPASLILLQQQ 60  
 Db 1 MEVQLGLGRVYPPSTKYTGAFQNLFSQSVREVIONGPRHPEAASAPPASLILL 57  
 Qy 61 QQQ 120  
 Db 58 -----QQ 112  
 Qy 121 POSALECHPERGCVPEPAAVASKGLPQLPAPDPEDDASAPSTLSLIGTFFGLSSCS 180  
 Db 113 POSALECHPERGCVPEPAAVASKGLPQLPAPDPEDDASAPSTLSLIGTFFGLSSCS 172

Qy 181 ADLKDIILSEASTMQLLQQQQQQEAVSEGGSSGRAREASGAPTSSKDYLGTTISDNKE 240  
 Db 173 ADLKDIILSEASTMQLLQQQQQQEAVSEGGSSGRAREASGAPTSSKDYLGTTISDNKE 232  
 Qy 241 LCKAVSVSMGLGVEALEHLSPGQLRGDCMYAPLLGVPPAVRPTPCAPLAECGSLDD 300  
 Db 233 LCKAVSVSMGLGVEALEHLSPGQLRGDCMYAPLLGVPPAVRPTPCAPLAECGSLDD 292  
 Qy 301 AGKSTEDTAIEYSPFKGGYTKGLESGICGSAAGSSGTLPLSTLSLYKSGALDEAAA 360  
 Db 293 AGKSTEDTAIEYSPFKGGYTKGLESGICGSAAGSSGTLPLSTLSLYKSGALDEAAA 352  
 Qy 361 YQSRDYNNPLALAGPPPPPPHARIKLENPLDYGSANAAAAOQRYGDLASLHGAG 420  
 Db 353 YQSRDYNNPLALAGPPPPPPHARIKLENPLDYGSANAAAAOQRYGDLASLHGAG 412  
 Qy 421 AAGPGSGSPSAAASSSWHTLFTAEGQLYGPC--GGGGGGGGGGGGGGGGGGGGGG 477  
 Db 413 AAGPGSGSPSAAASSSWHTLFTAEGQLYGPCGGGGGGGGGGGGGGGGGGGGGG 472  
 Qy 478 AGAVAPYGYTRPPQGLAGQESDFTAPDVYVPGMVSRYPSPCTCVKSEMCPWMDSYSGP 537  
 Db 473 AEAVAPYGYTRPPQGLAGQESDFTAPDVYVPGMVSRYPSPCTCVKSEMCPWMDSYSGP 532  
 Qy 538 YGDMRLTARDHVLPIIDYFFPPQKTCCLICGDEASGCHYGALTGCGSKVFFKRAAEFGK 597  
 Db 533 YGDMRLTARDHVLPIIDYFFPPQKTCCLICGDEASGCHYGALTGCGSKVFFKRAAEFGK 592  
 Qy 598 LCASRNDCCTIDKFRKNCPSCLRLKCYEAGMTLGARKLKLGKLGKLOEGEASSTTSPT 657  
 Db 593 LCASRNDCCTIDKFRKNCPSCLRLKCYEAGMTLGARKLKLGKLGKLOEGEASSTTSPT 652  
 Qy 658 ETQKLTVSHIEGVECOPIFLNLEATEPGVVCAGHNDNPDSPFAALLSSINELGEROLV 717  
 Db 653 ETQKLTVSHIEGVECOPIFLNLEATEPGVVCAGHNDNPDSPFAALLSSINELGEROLV 712  
 Qy 718 HVVWKAKALPGFRLHVDQNAVIOYSWMGLMVFAMGWSFTVNSRMLYFAPDLVNEY 777  
 Db 713 HVVWKAKALPGFRLHVDQNAVIOYSWMGLMVFAMGWSFTVNSRMLYFAPDLVNEY 772  
 Qy 778 RMHKSRYMSQCVRMHLSQEGFWLQITPOEFLCMKALLFSIIPVGLKNOKEFDELWMN 837  
 Db 773 RMHKSRYMSQCVRMHLSQEGFWLQITPOEFLCMKALLFSIIPVGLKNOKEFDELWMN 832  
 Qy 838 YIKELDRIIACRKNPTSCSRFFVQLTKLDSVQPIARELHQFTFDLLIKSHMVSVDFFE 897  
 Db 833 YIKELDRIIACRKNPTSCSRFFVQLTKLDSVQPIARELHQFTFDLLIKSHMVSVDFFE 892  
 Qy 898 MNAETISVQVPKILSGKVPIPHQTQ 923  
 Db 893 MNAETISVQVPKILSGKVPIPHQTQ 918  
 RESULT 6  
 AAR12223  
 ID AAR12223 standard; Protein; 918 AA.  
 XX  
 AC AAR12223;  
 XX  
 DT 20-AUG-1991 (first entry)  
 XX  
 DE Human androgen receptor.  
 XX  
 KW hAR; DNA-binding protein; steroid hormone.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key  
 FT Domain  
 FT /label= "DNA-binding domain  
 FT /note= "cysteine-rich"  
 XX



CC starts from the second.

XX Sequence 919 AA;

```

Query Match      98.0%; Score 4814; DB 10; Length 919;
Best Local Similarity 98.4%; Pred. No. 3.5e-316;
Matches 912; Conservative 0; Mismatches 3; Indels 12; Gaps 3;

QY 1 MEVQLGLGRVYPRPSPKTYRGAFONLFQSVREVIQNGPRHPPEAASAAPPGASLLLLQQO 60
Db 1 MEVQLGLGRVYPRPSPKTYRGAFONLFQSVREVIQNGPRHPPEAASAAPPGASLLLL--- 57
QY 61 QOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQO 119
Db 58 -----QOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQO 112
QY 120 QPSALECHPERGCVPEPGAAVASKGLPQOLPAPDEDDSAAPSTLSLGGTFFGLSSC 179
Db 113 QPSALECHPERGCVPEPGAAVASKGLPQOLPAPDEDDSAAPSTLSLGGTFFGLSSC 172
QY 180 SADLKDILSEASTMQLLQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQO 239
Db 173 SADLKDILSEASTMQLLQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQO 232
QY 240 ELCKAVSVSMGLGVEALEHLSPEQOLRGDCMVAPLLGVPPAVRPTPCAPLAECKGSLDD 299
Db 233 ELCKAVSVSMGLGVEALEHLSPEQOLRGDCMVAPLLGVPPAVRPTPCAPLAECKGSLDD 292
QY 300 SACKSTEDTAEYSPFKGGYTKLEGESLCSGSAAGSSGTLELPSTLSLYKSGALDEAA 359
Db 293 SACKSTEDTAEYSPFKGGYTKLEGESLCSGSAAGSSGTLELPSTLSLYKSGALDEAA 352
QY 360 AYOSRDYINFPALAGPPLPPPPHARIKLENPLDYGSAWAAAAACRYDGLASLHGA 419
Db 353 AYOSRDYINFPALAGPPLPPPPHARIKLENPLDYGSAWAAAAACRYDGLASLHGA 412
QY 420 GAAGPGSGSPSAASSSWHTLFTAEGLYGPC---GGGGGGGGGGGGGGGGGGGGGGGGGG 476
Db 413 GAAGPGSGSPSAASSSWHTLFTAEGLYGPCGGGGGGGGGGGGGGGGGGGGGGGGGGGG 472
QY 477 EACAVAPYGYTRPPQGLAQESDFAPDVWYPGMVSRVYPSPTCVKSEMPWMDSYSG 536
Db 473 EACAVAPYGYTRPPQGLAQESDFAPDVWYPGMVSRVYPSPTCVKSEMPWMDSYSG 532
QY 537 PYGDMRLETARDHVLPIIDYFPPOKTCLICGDEASGCHYGALTCGCKVFPKRAAEKQK 596
Db 533 PYGDMRLETARDHVLPIIDYFPPOKTCLICGDEASGCHYGALTCGCKVFPKRAAEKQK 592
QY 597 YLCASRNDCTIDKFRKNCPSRLKCYEAGMTLGARKLKLGNLKLQEEGEASSTTSPT 656
Db 593 YLCASRNDCTIDKFRKNCPSRLKCYEAGMTLGARKLKLGNLKLQEEGEASSTTSPT 652
QY 657 EETTKLTVSHTEGECOPIFLNVLAEPTGVVCAHDNNQPDFAALLSSNLNGLERQL 716
Db 653 EETTKLTVSHTEGECOPIFLNVLAEPTGVVCAHDNNQPDFAALLSSNLNGLERQL 712
QY 717 VHVWAKALPGFRLNHLVDQMAVTOXSWGLMVFAMGWRSTFVNSRMLYEAPDLVFN 776
Db 713 VHVWAKALPGFRLNHLVDQMAVTOXSWGLMVFAMGWRSTFVNSRMLYEAPDLVFN 772
QY 777 YRMHKSRYMSQCVNRHLSQEGWLQITPOEFLCMKALLFSIIPVDGLKNQKFFDELRM 836
Db 773 YRMHKSRYMSQCVNRHLSQEGWLQITPOEFLCMKALLFSIIPVDGLKNQKFFDELRM 832
QY 837 NYIKELDRILACKRNKPTSCRRRYQLTKLDSVQPTARELHFTFDLLIKSHMWSVDFP 896
Db 833 NYIKELDRILACKRNKPTSCRRRYQLTKLDSVQPTARELHFTFDLLIKSHMWSVDFP 892
QY 897 EMMAEIIISVQPKILSGKVKPIYFHTQ 923
Db 893 EMMAEIIISVQPKILSGKVKPIYFHTQ 919
```

RESULT 8

```

AAP91006
ID AAP91006 standard; protein; 902 AA.
XX
XX AAP91006;
AC
XX
XX 28-FEB-1990 (first entry)
DT
XX
XX Rat androgen receptor DNA clone.
DE
XX
XX Androgen receptor; TR2 polypeptide;
KW
XX
XX Rat.
OS
XX
XX
XX Key Location/Qualifiers
FH Region 1..902
FT /tag= a
FT /product=98 kD polypeptide
FT Region 170..902
FT /tag= b
FT /product=79 kD polypeptide
XX
XX WO8909223-A.
XX
XX 05-OCT-1989.
XX
XX 24-MAR-1989; 89WO-US01238.
XX
XX 30-MAR-1988; 88US-0176107.
XX
XX (ARCH-) ARCH DEVELOPMENT CORP.
XX
XX Liao S, Chang C;
XX
XX WPI: 1989-309501/42.
XX
XX N-PSDB; AAN91578.
XX
XX New DNA encoding new androgen receptor and TR2 polypeptide(s) - able
XX to bind DNA, and derived antibodies, useful for receptor assay and
XX purification.
XX
XX Claim 8; Fig 3; 60pp; English.
XX
XX The protein is used to raise antibodies for receptor assays and for
XX affinity purification.
XX
XX The 98 kD product starts at the first Met codon; the 79 kD product
XX starts from the second.
XX
XX Sequence 902 AA;
```

```

Query Match      85.5%; Score 4201.5; DB 10; Length 502;
Best Local Similarity 84.6%; Pred. No. 7.2e-275;
Matches 796; Conservative 36; Mismatches 52; Indels 57; Gaps 4;

QY 1 MEVQLGLGRVYPRPSPKTYRGAFONLFQSVREVIQNGPRHPPEAASAAPPGASLLLLQQO 60
Db 1 MEVHLGLGRVYPRPSPKTYRGAFONLFQSVREVIQNGPRHPPEAASAAPPGASLLLL 60
QY 61 QOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQO 119
Db 55 -----QOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQO 96
QY 120 QPSALECHPERGCVPEPGAAVASKGLPQOLPAPDEDDSAAPSTLSLGGTFFGLSSC 179
Db 97 QOQASASGHPESGCLPEPGAATAPGKLPQOPAPPDQDDSAAPSTLSLGGTFFGLSSC 156
QY 180 SADLKDILSEASTMQLL-----QOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQO 222
Db 157 SADLKDILSEASTMQLLQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQO 216
QY 223 SKDNLGGTSTISDNKELCKAVSVSMGLGVEALEHLSPEQOLRGDCMVAPLLGVPPAVR 282
Db 217 SKDSYLOGNSTISDSAKELCKAVSVSMGLGVEALEHLSPEQOLRGDCMVAPLLGVPPAVR 276
```









RESULT 12  
AAG68238 standard; Protein; 839 AA.  
XX ID AAG68238;  
XX AC AAG68238;  
XX DT 08-FEB-2002 (first entry)  
XX DE Fused androgen receptor (AR) protein SEQ ID NO:11.  
XX KW Human; androgen receptor; AR; fused androgen receptor protein;  
KW fusion androgen receptor protein; sugar-combining protein;  
KW maltose-combining protein.  
XX OS Chimeric - Homo sapiens.  
OS Chimeric - Unidentified.  
XX PN JP2001252080-A.  
XX PD 18-SEP-2001.  
XX PF 13-MAR-2000; 2000JP-0069030.  
XX PR 13-MAR-2000; 2000JP-0069030.  
XX PA (TOYM ) TOYOBO KK.  
XX WPI: 2002-029658/04.  
DR N-PSDB; ABA01683.  
XX PT New polypeptide for screening drugs, comprises an androgen receptor  
PT protein fused with a sugar-combining protein -  
XX PS Claim 8; Page 11-13; 16pp; Japanese.  
XX CC The present invention describes a fused androgen receptor (AR) protein  
CC prepared by fusing an androgen receptor protein with a sugar-combining  
CC protein. Also described are: (1) a gene encoding the above fused AR  
CC protein; (2) a vector carrying the above gene; (3) a transformant in  
CC which the above vector is introduced to a microbe and a gene encoding  
CC the fused AR protein is expressed; (4) the preparation of a fused AR  
CC protein in which the above transformant is cultured and the fused AR  
CC protein is collected from the resultant culture; and (5) a reagent for  
CC detecting the presence of interaction with a ligand containing the  
CC above fused AR protein, a solvent for dissolving chemical substances  
CC and a diluent liquid of the dissolved chemical substances. The fusion  
CC protein can be used for screening drugs. The present sequence represents  
CC the AR protein and sugar-combining protein fusion protein from the  
CC present invention.  
XX SQ Sequence 839 AA;  
Query Match 48.9%; Score 2401; DB 23; Length 839;  
Best Local Similarity 99.3%; Pred. No. 2e-153;  
Matches 446; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
Qy 475 GGEAGAVAPGYTRPPQGLAGQESDFTAPDWWPGMVSVPYSPPTCVKSEMGPMWDSY 534  
Db 391 GSEAGAVAPGYTRPPQGLAGQESDFTAPDWWPGMVSVPYSPPTCVKSEMGPMWDSY 450  
Qy 535 SGPGYDMRLTARDHVLPIIDYFPPOKTCICGDEASGCHYGALTCGSKVFFKRAAEGK 594  
Db 451 SGPGYDMRLTARDHVLPIIDYFPPOKTCICGDEASGCHYGALTCGSKVFFKRAAEGK 510  
Qy 595 QKYLCAASNDCTIDKFRKNCPSRLRKYEAGMTLGARKLKLGNLKLQEEGASSTTS 654  
Db 511 QKYLCAASNDCTIDKFRKNCPSRLRKYEAGMTLGARKLKLGNLKLQEEGASSTTS 570  
Qy 655 PTEETQKLTVSHIEGYEQPIFLNVLAEIPGVVCAAGHNNQPDFAALLSSNLGEL 714  
Db 571 PTEETQKLTVSHIEGYEQPIFLNVLAEIPGVVCAAGHNNQPDFAALLSSNLGEL 630

XX OS Homo sapiens.  
XX PN W09926966-A2.  
XX PD 03-JUN-1999.  
XX PF 25-NOV-1998; 98WO-US25296.  
XX PR 26-NOV-1997; 97US-0980115.  
XX PA (REBC ) UNIV CALIFORNIA.  
XX PI Aprilletti JW, Baxter JD, Fletterick RJ, Kushner PJ;  
PI Scanlan TS, Shiau AK, Wagner RL, West BL;  
XX WPI: 1999-357810/30.  
XX PT Modulating activity of a thyroid hormone receptor  
XX PS Disclosure; Fig 3H-R; 447pp; English.  
XX CC The invention relates to a method for modulating activity of a thyroid  
CC hormone receptor that comprises administration of an aromatic compound  
CC which fits spatially and preferentially into a thyroid hormone ligand  
CC binding domain. The aromatic compound (of a specified formula) can be  
CC used to increase alpha-glycerophosphate dehydrogenase (GPDH) levels, at  
CC levels which do not significantly modify cardiac GPDH levels and are  
CC indicated in the treatment of obesity. The compound also lower total  
CC plasma cholesterol and triglyceride levels and can be used as anti-  
CC hypertriglyceridaemic agents. The compound may also be used for treating  
CC atherosclerosis and may be indicated in thyroid hormone replacement  
CC therapy in patients with compromised cardiac function. Sequences  
CC AAY21621- 636 amino acid sequences of ligand binding domains of several  
CC members of the nuclear receptor superfamily.  
XX SQ Sequence 452 AA;  
Query Match 49.5%; Score 2429; DB 20; Length 452;  
Best Local Similarity 99.8%; Pred. No. 1.2e-155;  
Matches 451; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 472 GGGGAGAVAPGYTRPPQGLAGQESDFTAPDWWPGMVSVPYSPPTCVKSEMGPMW 531  
Db 1 GGGGAGAVAPGYTRPPQGLAGQESDFTAPDWWPGMVSVPYSPPTCVKSEMGPMW 60  
Qy 532 DSYSGPYGDMRLTARDHVLPIIDYFPPOKTCICGDEASGCHYGALTCGSKVFFKRAA 591  
Db 61 DSYSGPYGDMRLTARDHVLPIIDYFPPOKTCICGDEASGCHYGALTCGSKVFFKRAA 120  
Qy 592 EGKQKYLCAASNDCTIDKFRKNCPSRLRKYEAGMTLGARKLKLGNLKLQEEGEASS 651  
Db 121 EGKQKYLCAASNDCTIDKFRKNCPSRLRKYEAGMTLGARKLKLGNLKLQEEGEASS 180  
Qy 652 TTSPTETQKLTVSHIEGYEQPIFLNVLAEIPGVVCAAGHNNQPDFAALLSSNL 711  
Db 181 TTSPTETQKLTVSHIEGYEQPIFLNVLAEIPGVVCAAGHNNQPDFAALLSSNL 240  
Qy 712 GERQLVHVVKAKALPGFRLNHLVDVDMQAVIQYSGMGLMVFAMGWSFTNVNSRMLYFAPD 771  
Db 241 GERQLVHVVKAKALPGFRLNHLVDVDMQAVIQYSGMGLMVFAMGWSFTNVNSRMLYFAPD 300  
Qy 772 LVFNEMRMKSRMYSQVCRMRHLSEQFGLQITPQEFCKMALLLSIIPVDGLKNQKFF 831  
Db 301 LVFNEMRMKSRMYSQVCRMRHLSEQFGLQITPQEFCKMALLLSIIPVDGLKNQKFF 360  
Qy 832 DELRMNVIKELDRITACKRNPTSCSRFFVOLTFLKLDVQPIARELHQFTFDLLIKSHMV 891  
Db 361 DELRMNVIKELDRITACKRNPTSCSRFFVOLTFLKLDVQPIARELHQFTFDLLIKSHMV 420  
Qy 892 SVDFPENMAELISVQVPKILSGKVKPIYFHTQ 923  
Db 421 SVDFPENMAELISVQVPKILSGKVKPIYFHTQ 452

QY 715 QLVHVYVWAKALPGFRNLHVDDQMAVIOYSWMGLMVFAMGWRSTNNVNSRMLYFAPDLVF 774  
Db 631 QLVHVYVWAKALPGFRNLHVDDQMAVIOYSWMGLMVFAMGWRSTNNVNSRMLYFAPDLVF 690  
QY 775 NEYRMHKSRYMSQCVRMHLSQEGWLOITPQEFCLMKALLLSIIPVDGLKNOKFFDEL 834  
Db 691 NEYRMHKSRYMSQCVRMHLSQEGWLOITPQEFCLMKALLLSIIPVDGLKNOKFFDEL 750  
QY 835 RMNYIKELDRIIACKRNPTSCSRFFYQLTKLLDSVQPIARELHQFTFDLLIKSHMVSVD 894  
Db 751 RMNYIKELDRIIACKRNPTSCSRFFYQLTKLLDSVQPIARELHQFTFDLLIKSHMVSVD 810  
QY 895 FPEMAEIIISVQVVKILSGVKPIYFHTQ 923  
Db 811 FPEMAEIIISVQVVKILSGVKPIYFHTQ 839

RESULT 13  
ABB83821  
ID ABB83821 standard; Protein; 388 AA.  
XX  
AC ABB83821;  
XX  
DT 13-SEP-2002 (first entry)  
XX  
DE Human androgen receptor variant AR42 SEQ ID NO 2.  
XX  
KW Human; androgen receptor; receptor; AR; AR42; AR32; tumour; cancer;  
KW steroid response element; prostate cancer; testis; gene therapy;  
KW hormone therapy; cytostatic; contraceptive.  
XX  
OS Homo sapiens.  
XX  
PN EP1213300-A1.  
XX  
PD 12-JUN-2002.  
XX  
PE 26-OCT-2001; 2001EP-0250379.  
XX  
PR 30-NOV-2000; 2000DE-1061161.  
XX  
PA (SCHD ) SCHERING AG.  
XX  
PI Ahrens-Fath I, Haendler B;  
XX  
XW WPI; 2002-530575/57.  
DR N-PSDB; ABB85656.  
XX  
PT New nucleic acid encoding variant forms of androgen receptor; useful  
PT for diagnosis and treatment of prostatic cancer, also related proteins  
PT and antibodies  
XX  
PS Claim 5; Page 9-11; 25pp; German.  
XX  
CC The invention relates to a nucleic acid (I) that encodes an androgen  
CC receptor (AR) variant AR42 (ABB85656) or AR32 (ABB85657) or its  
CC equivalents or a sequence that hybridises to them under stringent  
CC conditions. Polypeptides (II, ABB83821-ABB83822) expressed by (I), can  
CC bind androgens and other ligands and form heterodimers which can bind to  
CC steroid response elements in target genes but do not induce activation,  
CC so act as repressors of the known AR.(II) are used to raise specific  
CC antibodies. (I) are used for recombinant production of (II) and as probes  
CC for detecting (I)-related nucleic acid in tumour tissue. Also (I), (II),  
CC a specific peptide and cells transfected with (I)-containing vectors, are  
CC useful for identifying effectors of (II), specifically antiandrogenic  
CC agents potentially useful for treating androgen-related diseases, e.g.  
CC cancer of prostate or testis and as male contraceptives. (I) can be used  
CC similarly in gene therapy. Antibodies to (II) are used to detect or  
CC quantify (II) in tumour tissue, e.g. to determine if resistance to  
CC hormone therapy is the result of altered expression of (II).

Sequence 388 AA;  
SQ

Query Match 41.3%; Score 2029.5; DB 23; Length 388;  
Best Local Similarity 97.2%; Pred. No. 8.7e-129;  
Matches 383; Conservative 1; Mismatches 1; Indels 9; Gaps 1;  
QY 530 WMDSYSGPYGDMRLLETARDHVLPIIDYPPQKTCICGDEASGCHYGALTGSCVKFFKR 589  
Db 4 WLHS-----LETARDHVLPIIDYPPQKTCICGDEASGCHYGALTGSCVKFFKR 54  
QY 590 AAEGRQKYLCAARNDCITDKFRKNCPCSRRLKCYEAGMTLGARKLKLGNLKLQEEGEA 649  
Db 55 AAEGRQKYLCAARNDCITDKFRKNCPCSRRLKCYEAGMTLGARKLKLGNLKLQEEGEA 114  
QY 650 STTSPTETTKOKLTIVSHIEGYECQPIFLNLEAIEPVGVCAGHDNNQPDFAALLSSLN 709  
Db 115 STTSPTETTKOKLTIVSHIEGYECQPIFLNLEAIEPVGVCAGHDNNQPDFAALLSSLN 174  
QY 710 ELGERQLVHVYVWAKALPGFRNLHVDDQMAVIOYSWMGLMVFAMGWRSTNNVNSRMLYFA 769  
Db 175 ELGERQLVHVYVWAKALPGFRNLHVDDQMAVIOYSWMGLMVFAMGWRSTNNVNSRMLYFA 234  
QY 770 PDLVENEYRMHKSRYMSQCVRMHLSQEGWLOITPQEFCLMKALLLSIIPVDGLKNOK 829  
Db 235 PDLVENEYRMHKSRYMSQCVRMHLSQEGWLOITPQEFCLMKALLLSIIPVDGLKNOK 294  
QY 830 FEDELRMNYIKELDRIIACKRNPTSCSRFFYQLTKLLDSVQPIARELHQFTFDLLIKSH 889  
Db 295 FEDELRMNYIKELDRIIACKRNPTSCSRFFYQLTKLLDSVQPIARELHQFTFDLLIKSH 354  
QY 890 MVSVDFFPEMAEIIISVQVVKILSGVKPIYFHTQ 923  
Db 355 MVSVDFFPEMAEIIISVQVVKILSGVKPIYFHTQ 388

RESULT 14  
ABB83822  
ID ABB83822 standard; Protein; 294 AA.  
XX  
AC ABB83822;  
XX  
DT 13-SEP-2002 (first entry)  
XX  
DE Human androgen receptor variant AR32 SEQ ID NO 4.  
XX  
KW Human; androgen receptor; receptor; AR; AR42; AR32; tumour; cancer;  
KW steroid response element; prostate cancer; testis; gene therapy;  
KW hormone therapy; cytostatic; contraceptive.  
XX  
OS Homo sapiens.  
XX  
PN EP1213300-A1.  
XX  
PD 12-JUN-2002.  
XX  
PE 26-OCT-2001; 2001EP-0250379.  
XX  
PR 30-NOV-2000; 2000DE-1061161.  
XX  
PA (SCHD ) SCHERING AG.  
XX  
PI Ahrens-Fath I, Haendler B;  
XX  
XW WPI; 2002-530575/57.  
DR N-PSDB; ABB85657.  
XX  
PT New nucleic acid encoding variant forms of androgen receptor; useful  
PT for diagnosis and treatment of prostatic cancer, also related proteins  
PT and antibodies  
XX  
PS Claim 5; Page 11-12; 25pp; German.  
XX  
CC The invention relates to a nucleic acid (I) that encodes an androgen  
CC receptor (AR) variant AR42 (ABB85656) or AR32 (ABB85657) or its

CC equivalents or a sequence that hybridises to them under stringent  
CC conditions. Polypeptides (II, AB83821-AB83822) expressed by (I), can  
CC bind androgens and other ligands and form heterodimers which can bind to  
CC steroid response elements in target genes but do not induce activation,  
CC so act as repressors of the known AR. (II) are used to raise specific  
CC antibodies. (I) are used for recombinant production of (II) and as probes  
CC for detecting (I)-related nucleic acid in tumour tissue. Also (I), (II),  
CC a specific peptide and cells transfected with (I)-containing vectors, are  
CC useful for identifying effectors of (II), specifically antiandrogenic  
CC agents potentially useful for treating androgen-related diseases, e.g.  
CC cancer of prostate or testis and as male contraceptive. (I) can be used  
CC similarly in gene therapy. Antibodies to (II) are used to detect or  
CC quantify (II) in tumour tissue, e.g. to determine if resistance to  
CC hormone therapy is the result of altered expression of (II).

XX Sequence 294 AA;  
SQ  
Query Match 30.4%; Score 1493.5; DB 23; Length 294;  
Best Local Similarity 100.0%; Pred. No. 9e-93;  
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 543 LETARDHVLPIIDYFPQKTLICGDEASGCHYGALTGCGSKVFFKRAEKGKYLCSAR 602  
DB 8 LETARDHVLPIIDYFPQKTLICGDEASGCHYGALTGCGSKVFFKRAEKGKYLCSAR 67  
QY 603 NCTIDFRKNCPSCLRLKCYEAGTGLGARKLKLGNLKLQEGEASSTTPTETTK 662  
DB 68 NCTIDFRKNCPSCLRLKCYEAGTGLGARKLKLGNLKLQEGEASSTTPTETTK 127  
QY 663 LTVSHIEGYECOPILNVLAEIEPGVVCAGHDNNQPDFAALLSSNLGELQVHVYVKW 722  
DB 128 LTVSHIEGYECOPILNVLAEIEPGVVCAGHDNNQPDFAALLSSNLGELQVHVYVKW 187  
QY 723 AKALPGFRNLHVDQMAVIOYSWGLMVFAMGWRSTNNVNSRMLYFAPDLVFNEMRHS 782  
DB 188 AKALPGFRNLHVDQMAVIOYSWGLMVFAMGWRSTNNVNSRMLYFAPDLVFNEMRHS 247  
QY 793 RMYSOVVRMRLHSQEFGLQITPOEFLCMKALLFSI 819  
DB 248 RMYSOVVRMRLHSQEFGLQITPOEFLCMKALLFSI 284

RESULT 15  
ID AAR12230 standard; Protein; 630 AA.  
XX  
AC AAR12230;  
XX  
DT 20-AUG-1991 (first entry)  
XX  
DE TrpE/androgen receptor DNA-binding domain fusion protein.  
XX androgen receptor; AR; DNA-binding protein; steroid hormone.  
XX Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Protein 1..323  
FT /label= 33kD trpE protein  
FT Region 324..334  
FT /label= 11 amino acid linker  
FT Protein 335..613  
FT /label= 29kD protein incl. AR DNA-binding domain  
FT Region 614..630  
FT /label= 17 amino acid linker  
XX  
PN WO9107423-A.  
XX  
PD 30-MAY-1991.  
XX  
PF 19-OCT-1990; 90WO-US06015.  
XX  
PR 17-NOV-1989; 89US-0439775.

XX (ARCH-) ARCH DEV CORP.  
PA Liao S, Chang C;  
XX WPI; 1991-178048/24.  
XX N-PSDB; AAQ12008.  
DR Androgen receptor and TR2 DNA binding proteins - DNA sequences  
DR and antibodies for detection and quantification methods  
XX Example 13; Fig 10; 79pp; English.  
PS To express an androgen receptor fusion protein in E.coli, the PATH  
CC expression system was used. The trpE is insoluble so partially  
CC purified induced fusion protein is obtained by simply lysing the  
CC E.coli and precipitating the insoluble fusion protein. The fusion  
CC protein was used for immunisation to obtain monoclonal anti-AR  
CC antibodies.  
XX  
SQ Sequence 630 AA;  
Query Match 29.7%; Score 1459; DB 12; Length 630;  
Best Local Similarity 79.9%; Pred. No. 5.1e-90;  
Matches 286; Conservative 17; Mismatches 31; Indels 24; Gaps 6;  
QY 515 VYPSPPTCV-----KSEMGPMW-----DS-----YSGPYGDMRLE-TARDHVLPIIDYFPP 559  
DB 272 LPCPSPLAAVYVLLKSNPSYPMFFMQDNDFTLFGASPESSLYKIDATSRQIIPGRARIRA 331  
QY 560 QKTCILCGDEASGCHYGALTGCGSKVFFKRAEKGKYLCSARNDCTIDKFRKNCPSCR 619  
DB 332 RPG--ICGDEASGCHYGALTGCGSKVFFKRAEKGKYLCSARNDCTIDKFRKNCPSCR 389  
QY 620 LRKCYEAGMTGLGARKLKLGNLKLQEGEASSTTPTETTKLTVSHIEGYECOPILN 679  
DB 390 LRKCYEAGMTGLGARKLKLGNLKLQEGEASSTTPTETTKLTVSHIEGYECOPILN 449  
QY 680 VLEAIEPGVVCAGHDNNQPDFAALLSSNLGELQVHVYVKWAKALPGFRNLHVDQMA 739  
DB 450 VLEAIEPGVVCAGHDNNQPDFAALLSSNLGELQVHVYVKWAKALPGFRNLHVDQMA 509  
QY 740 VIOYSWGLMVFAMGWRSTNNVNSRMLYFAPDLVFNEMRHSRMYSOVVRMRLHSQEF 799  
DB 510 VIOYSWGLMVFAMGWRSTNNVNSRMLYFAPDLVFNEMRHSRMYSOVVRMRLHSQEF 569  
QY 800 WLQITPOEFLCMKALLFSIIPVDGLKNOKFFDELRMNVIKELDRIIACKRKNPTSCS 857  
DB 570 WLQITPOEFLCMKALLFSIIPVDGLKNOKFFDELRMNVIKELDRIIACKRKNPTSCS 620

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Job time : 49 secs